RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

<u>09/476,485B</u>
1FW/6
3/21/05

ENTERED



IFW16

RAW SEQUENCE LISTING DATE: 03/21/2005
PATENT APPLICATION: US/09/476,485B TIME: 14:12:04

Input Set : A:\10823619.app

Output Set: N:\CRF4\03212005\I476485B.raw

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4 <110> APPLICANT: COLUCCI, M. GABRIELLA
        CHRISPEELS, MAARTEN J.
 5
        MOORE, JEFFREY G.
 6
 8 <120> TITLE OF INVENTION: PROGENITOR CELL PRESERVATION FACTORS AND METHODS FOR
        AND PRODUCTS OF THEIR USE
 9
11 <130> FILE REFERENCE: PHY-003US1/108236.119US1
13 <140> CURRENT APPLICATION NUMBER: 09/476,485B
14 <141> CURRENT FILING DATE: 1999-12-30
16 <150> PRIOR APPLICATION NUMBER: 08/881,189
17 <151> PRIOR FILING DATE: 1997-06-24
19 <160> NUMBER OF SEQ ID NOS: 61
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 939
25 <212> TYPE: DNA
26 <213> ORGANISM: Artificial Sequence
28 <220> FEATURE:
29 <223> OTHER INFORMATION: D1-FRIL.
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                                                                         120
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37 aaccctgtga gttctagtgc gggaagagtg ttatattctg caccattgcg cctttgggaa
                                                                         180
39 gactctgcgg tattgacaag ctttgacacc attatcaact ttgaaatctc aacaccttac
                                                                         240
41 acttctcgta tagctgatgg cttggccttc ttcattgcac cacctgactc tgtcatcagt
                                                                         300
43 tatcatggtg gttttcttgg actctttccc aacgcaaaca ctctcaacaa ctcttccacc
                                                                         360
45 tctgaaaacc aaaccaccac taaggctgca tcaagcaacg ttgttgctgt tgaatttgac
                                                                         420
47 acctatetta atecegatta tggtgateca aactacatae acateggaat tgaegteaae
                                                                         480
49 tctattagat ccaaggtaac tgctaagtgg gactggcaaa atgggaaaat agccactgca
                                                                         540
                                                                         600
51 cacattagct ataactctgt ctctaaaaga ctatctgtta ctagttatta tgctgggagt
53 aaacctgcga ctctctccta tgatattgag ttacatacag tgcttcctga atgggtcaga
                                                                         660
55 gtagggttat ctgcttcaac tggacaagat aaagaaagaa ataccgttca ctcatggtct
                                                                         720
57 ttcacttcaa gcttgtggac caatgtggcg aagaaggaga atgaaaacaa gtatattaca
                                                                         780
59 agaggcgttc tgtgatgata tatgtgtatc aatgattttc tatgttataa gcatgtaatg
                                                                         840
61 tgcgatgagt caataatcac aagtacagtg tagtacttgt atgttgtttg tgtaagagtc
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63 agtttgcttt taataataac aagtgcagtt agtacttgt
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68 <211> LENGTH: 264
69 <212> TYPE: PRT
70 <213> ORGANISM: Artificial Sequence
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73 <223> OTHER INFORMATION: D1-FRIL.
76 <400> SEQUENCE: 2
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77 Ala Gln Ser Leu Ser Phe Ser Phe Thr Lys Phe Asp Pro Asn Gln Glu

Input Set : A:\10823619.app

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81
84
86 Arg Val Leu Tyr Ser Ala Pro Leu Arg Leu Trp Glu Asp Ser Ala Val
87
89 Leu Thr Ser Phe Asp Thr Ile Ile Asn Phe Glu Ile Ser Thr Pro Tyr 90 65
90 65 70 75 80 92 Thr Ser Arg Ile Ala Asp Gly Leu Ala Phe Phe Ile Ala Pro Pro Asp 93 85 90 95 95 Ser Val Ile Ser Tyr His Gly Gly Phe Leu Gly Leu Phe Pro Asn Ala 100 105 110 98 Asn Thr Leu Asn Asn Ser Ser Thr Ser Glu Asn Gln Thr Thr Thr Lys 99 115 120 125 101 Ala Ala Ser Ser Asn Val Val Ala Val Glu Phe Asp Thr Tyr Leu Asn 102 130 135 140 104 Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His Ile Gly Ile Asp Val Asn 105 145 150 150 155 160 107 Ser Ile Arg Ser Lys Val Thr Ala Lys Trp Asp Trp Gln Asn Gly Lys 108 165 170 175 100 Ile Ala Thr Ala His Ile Ser Tyr Asn Ser Val Ser Lys Arg Leu Ser 111 180 185 190 113 Val Thr Ser Tyr Tyr Ala Gly Ser Lys Pro Ala Thr Leu Ser Tyr Asp 114 195 200 205 116 Ile Glu Leu His Thr Val Leu Pro Glu Trp Val Arg Val Gly Leu Ser 117 210 119 Ala Ser Thr Gly Gln Asp Lys Glu Arg Asn Thr Val His Ser Trp Ser 120 225 230 255 125 Lys Tyr Ile Thr Arg Gly Val Leu 126 260 129 <210 SEQ ID NO: 3
92 Thr Ser Arg Ile Ala Asp Gly Leu Ala Phe Phe Ile Ala Pro Pro Asp 85 90 95 95 Ser Val Ile Ser Tyr His Gly Gly Phe Leu Gly Leu Phe Pro Asn Ala 100 105 110 98 Asn Thr Leu Asn Asn Ser Ser Thr Ser Glu Asn Gln Thr Thr Thr Lys 120 125 101 Ala Ala Ser Ser Asn Val Val Ala Val Glu Phe Asp Thr Tyr Leu Asn 102 130 135 140 104 Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His Ile Gly Ile Asp Val Asn 105 145 150 150 160 107 Ser Ile Arg Ser Lys Val Thr Ala Lys Trp Asp Trp Gln Asn Gly Lys 165 165 170 175 110 Ile Ala Thr Ala His Ile Ser Tyr Asn Ser Val Ser Lys Arg Leu Ser 111 180 180 185 190 113 Val Thr Ser Tyr Tyr Ala Gly Ser Lys Pro Ala Thr Leu Ser Tyr Asp 205 116 Ile Glu Leu His Thr Val Leu Pro Glu Trp Val Arg Val Gly Leu Ser 215 220 119 Ala Ser Thr Gly Gln Asp Lys Glu Arg Asn Thr Val His Ser Trp Ser 220 122 Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys Lys Glu Asn Glu Asn 245 250 255 125 Lys Tyr Ile Thr Arg Gly Val Leu 126 260 129 <210> SEQ ID NO: 3
93
95 Ser Val Ile Ser Tyr His Gly Gly Phe Leu Gly Leu Phe Pro Asn Ala 96
96
99
101 Ala Ala Ser Ser Asn Val Val Ala Val Glu Phe Asp Thr Tyr Leu Asn 102
102
104 Pro Asp Tyr Gly Asp Pro Asn Tyr Ile His Ile Gly Ile Asp Val Asn 160 105 145
105 145
107 Ser Ile Arg Ser Lys Val Thr Ala Lys Trp Asp Trp Gln Asn Gly Lys 108
108
110 Ile Ala Thr Ala His Ile Ser Tyr Asn Ser Val Ser Lys Arg Leu Ser 111
111
113 Val Thr Ser Tyr Tyr Ala Gly Ser Lys Pro Ala Thr Leu Ser Tyr Asp 114
116 Ile Glu Leu His Thr Val Leu Pro Glu Trp Val Arg Val Gly Leu Ser 117 210 215 220 119 Ala Ser Thr Gly Gln Asp Lys Glu Arg Asn Thr Val His Ser Trp Ser 120 225 230 235 240 122 Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys Lys Glu Asn Glu Asn 123 245 250 255 125 Lys Tyr Ile Thr Arg Gly Val Leu 126 260 129 <210> SEQ ID NO: 3
117
119 Ala Ser Thr Gly Gln Asp Lys Glu Arg Asn Thr Val His Ser Trp Ser 120 225 230 235 240 122 Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys Lys Glu Asn Glu Asn 123 245 250 255 125 Lys Tyr Ile Thr Arg Gly Val Leu 126 260 129 <210> SEQ ID NO: 3
120 225 230 235 240 122 Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys Lys Glu Asn Glu Asn 123 245 250 255 125 Lys Tyr Ile Thr Arg Gly Val Leu 126 260 129 <210> SEQ ID NO: 3
122 Phe Thr Ser Ser Leu Trp Thr Asn Val Ala Lys Lys Glu Asn Glu Asn 123 245 250 255 125 Lys Tyr Ile Thr Arg Gly Val Leu 126 260 129 <210> SEQ ID NO: 3
123 245 250 255 125 Lys Tyr Ile Thr Arg Gly Val Leu 126 260 129 <210> SEQ ID NO: 3
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126 260 129 <210> SEQ ID NO: 3
130 <211> LENGTH: 1005
131 <212> TYPE: DNA
132 <213> ORGANISM: Artificial Sequence
134 <220> FEATURE:
135 <223> OTHER INFORMATION: Nucleic acid sequence of the naturally-occurring 136 D1-FRIL protein.
139 <400> SEQUENCE: 3
140 atggetteet ceaacttact caccetagee etetteettg tgetteteae ecaegeaaac 60
142 tragergeac agtrattgtc atttagtttc accaagtttg atcctaacca agaggatett 120
144 atcttccaag gtcatgccac ttctacaaac aatgtcttac aagtcaccaa gttagacagt 180
146 gcaggaaacc ctgtgagttc tagtgcggga agagtgttat attctgcacc attgcgcctt 240
148 tgggaagact ctgcggtatt gacaagcttt gacaccatta tcaactttga aatctcaaca 300
150 ccttacactt ctcgtatagc tgatggcttg gccttcttca ttgcaccacc tgactctgtc 360
152 atcagttate atggtggttt tettggaete ttteceaacg caaacactet caacaactet 420
154 tocacctotg aaaaccaaac caccactaag gotgoatcaa goaacgttgt tgotgttgaa 480

Input Set : A:\10823619.app

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156 tttgacacct atcttaatcc cgattatggt gatccaaact acatacacat cggaattgac
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158 gtcaactcta ttagatccaa ggtaactgct aagtgggact ggcaaaatgg gaaaatagcc
                                                                          600
160 actgcacaca ttagctataa ctctgtctct aaaagactat ctgttactag ttattatgct
                                                                          660
                                                                          720
162 gggagtaaac ctgcgactct ctcctatgat attgagttac atacagtgct tcctgaatgg
                                                                          780
164 qtcaqaqtaq qqttatctqc ttcaactqqa caaqataaaq aaagaaatac cqttcactca
166 tggtctttca cttcaagctt gtggaccaat gtggcgaaga aggagaatga aaacaagtat
                                                                          840
168 attacaagag gcgttctgtg atgatatatg tgtatcaatg attttctatg ttataagcat
                                                                          900
                                                                          960
170 gtaatgtgcg atgagtcaat aatcacaagt acagtgtagt acttgtatgt tgtttgtgta
172 agagtcagtt tgcttttaat aataacaagt gcagttagta cttgt
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175 <210> SEQ ID NO: 4
176 <211> LENGTH: 22
177 <212> TYPE: PRT
178 <213> ORGANISM: Artificial Sequence
180 <220> FEATURE:
181 <223> OTHER INFORMATION: Signal sequence from the FRIL family isolated from
         Dolichos lab lab
185 <400> SEOUENCE: 4
186 Met Ala Ser Ser Asn Leu Leu Thr Leu Ala Leu Phe Leu Val Leu Leu
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                                        10
189 Thr His Ala Asn Ser Ala
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190
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 914
195 <212> TYPE: DNA
196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: PV-FRIL.
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205 caaggtgatg ccacttctac aaacaatgtc ttacaactca ctaagttaga cagtggagga
                                                                          120
207 aaccetgtgg gtgctagtgt gggaagagtg ttattetetg caccatttea tetttgggaa
                                                                          180
209 aactctatgg cagtgtcaag ctttgaaact aatctcacca ttcaaatctc aacacctcac
                                                                          240
211 ccttattatg cagctgatgg ctttgccttc ttccttgcac cacatgacac tgtcatccct
                                                                          300
                                                                          360
213 ccaaattett ggggcaaatt cettggacte tactcaaacg ttttcagaaa etcececace
                                                                          420
215 tctgaaaacc aaaqctttqq tqatqtcaat actgactcaa qagttqttqc tqtcgaattt
217 gacaccttcc ctaatgccaa tattgatcca aattacagac acattggaat cgatgtgaac
                                                                          480
219 tctattaagt ccaaggaaac tgctaggtgg gagtggcaaa atgggaaaac ggccactgca
                                                                          540
221 cgcatcagct ataactctgc ctctaaaaaa tcaactgtta ctacgtttta tcctgqqatq
                                                                          600
223 gaagttgtgg ctctctccca tgatgttgac ttacatgcag agcttcctga atgggttaga
                                                                          660
225 gtagggttat ctgcttcaac tggagaggag aaacaaaaaa ataccattat ctcatggtct
                                                                          720
227 ttcacttcaa gcttgaagaa caacgaggtg aaggagccga aagaagacat gtatattgca
                                                                          780
                                                                          840
229 aacgttgtgc gatcatatac atggatcaat gacgttctat cttatataag caataaataa
231 atgtatgatg cactcaataa taatcacaag tacgtacggt gtagtacttg tatgttgttt
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                                                                          914
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238 <211> LENGTH: 279
239 <212> TYPE: PRT
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
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Input Set : A:\10823619.app

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                                    25
253 Leu Thr Lys Leu Asp Ser Gly Gly Asn Pro Val Gly Ala Ser Val Gly
            35
                                40
256 Arg Val Leu Phe Ser Ala Pro Phe His Leu Trp Glu Asn Ser Met Ala
257
                            55
259 Val Ser Ser Phe Glu Thr Asn Leu Thr Ile Gln Ile Ser Thr Pro His
                        70
                                            75
262 Pro Tyr Tyr Ala Ala Asp Gly Phe Ala Phe Phe Leu Ala Pro His Asp
                    85
                                        90
265 Thr Val Ile Pro Pro Asn Ser Trp Gly Lys Phe Leu Gly Leu Tyr Ser
                                    105
268 Asn Val Phe Arg Asn Ser Pro Thr Ser Glu Asn Gln Ser Phe Gly Asp
                                120
                                                     125
            115
271 Val Asn Thr Asp Ser Arg Val Val Ala Val Glu Phe Asp Thr Phe Pro
                            135
274 Asn Ala Asn Ile Asp Pro Asn Tyr Arg His Ile Gly Ile Asp Val Asn
                                            155
275 145
                        150
277 Ser Ile Lys Ser Lys Glu Thr Ala Arg Trp Glu Trp Gln Asn Gly Lys
                                        170
278
                    165
280 Thr Ala Thr Ala Arg Ile Ser Tyr Asn Ser Ala Ser Lys Lys Ser Thr
281
                180
                                    185
283 Val Thr Thr Phe Tyr Pro Gly Met Glu Val Val Ala Leu Ser His Asp
                                200
286 Val Asp Leu His Ala Glu Leu Pro Glu Trp Val Arg Val Gly Leu Ser
                            215
                                                 220
289 Ala Ser Thr Gly Glu Glu Lys Gln Lys Asn Thr Ile Ile Ser Trp Ser
290 225
                        230
                                            235
292 Phe Thr Ser Ser Leu Lys Asn Asn Glu Val Lys Glu Pro Lys Glu Asp
                    245
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295 Met Tyr Ile Ala Asn Val Val Arg Ser Tyr Thr Trp Ile Asn Asp Val
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303 <211> LENGTH: 678
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: YamFril partial mRNA sequence.
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314 aatgtcatac aactcaccaa gttagacagt aatggaaacc ctgtgagtac cagtgtggga
                                                                          120
316 agaqtqttat actctqcacc attqcqcctt tqqqaaagct ctacagtagt qtcaaccttt
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318 gagaccactt tcacctttca aatctcaaca ccttacacta gtcctcctgg tgatgggctc
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Input Set : A:\10823619.app

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320 gccttcttcc ttgcaccata tgacactgtc atccctccaa attctgctgg caatcttctt
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                                                                          360
322 ggactettte etaacttaaa tgetttaaga aactecacca ecagtaaaga aaccactatt
                                                                          420
324 gatgtcaatg ctgcatctaa caacgttgtt gccgttgaat ttgacaccta ccctaacgac
                                                                          480
326 aatattqqtq atccaaqata caaacacatt qqaatcqatq tcaactctat caggtccaag
328 gcaactgttg cgtgggactg gcaaaatggg aaaacagcca ctgcacacat cagctataac
                                                                          540
330 tctqcctcta aaaqactatc tqttactact ttttatcctq qgggtaaagc tgtgagtctt
                                                                          600
332 toccatgacg ttgageteac teaagtgett ceteaatgga ttagagtagg gttetetget
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334 tcaacaggat tagagaaa
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339 <211> LENGTH: 234
340 <212> TYPE: PRT
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343 <220> FEATURE:
344 <223> OTHER INFORMATION: YamFril deduced amino acid squence.
347 <400> SEQUENCE: 8
348 Ala Gln Ser Val Ser Phe Thr Phe Thr Lys Phe Asp Ser Asp Gln Lys
349 1
                                        10
351 Asp Leu Met Phe Gln Gly His Thr Ile Ser Ser Ser Asn Val Ile Gln
352
354 Leu Thr Lys Leu Asp Ser Asn Gly Asn Pro Val Ser Thr Ser Val Gly
                                40
355
            35
357 Arg Val Leu Tyr Ser Ala Pro Leu Arg Leu Trp Glu Ser Ser Thr Val
358
        50
360 Val Ser Thr Phe Glu Thr Thr Phe Thr Phe Gln Ile Ser Thr Pro Tyr
                                            75
361 65
                        70
363 Thr Ser Pro Pro Gly Asp Gly Leu Ala Phe Phe Leu Ala Pro Tyr Asp
                    85
366 Thr Val Ile Pro Pro Asn Ser Ala Gly Asn Leu Leu Gly Leu Phe Pro
                                    105
367
                100
369 Asn Leu Asn Ala Leu Arg Asn Ser Thr Thr Ser Lys Glu Thr Thr Ile
           115
                                120
372 Asp Val Asn Ala Ala Ser Asn Asn Val Val Ala Val Glu Phe Asp Thr
                            135
                                                 140
       130
375 Tyr Pro Asn Asp Asn Ile Gly Asp Pro Arg Tyr Lys His Ile Gly Ile
                        150
                                            155
378 Asp Val Asn Ser Ile Arg Ser Lys Ala Thr Val Ala Trp Asp Trp Gln
379
                    165
                                        170
                                                             175
381 Asn Gly Lys Thr Ala Thr Ala His Ile Ser Tyr Asn Ser Ala Ser Lys
382
                180
                                    185
384 Arg Leu Ser Val Thr Thr Phe Tyr Pro Gly Gly Lys Ala Val Ser Leu
           195
                                200
                                                     205
387 Ser His Asp Val Glu Leu Thr Gln Val Leu Pro Gln Trp Ile Arg Val
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                                                 220
       210
390 Gly Phe Ser Ala Ser Thr Gly Leu Glu Lys
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394 <210> SEQ ID NO: 9
395 <211> LENGTH: 15
396 <212> TYPE: PRT
397 <213> ORGANISM: Artificial Sequence
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Input Set : A:\10823619.app

Output Set: N:\CRF4\03212005\I476485B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; Xaa Pos. 14
Seq#:11; N Pos. 3,6,9,12,15,18,21
Seq#:12; N Pos. 3,6,9,15
Seq#:16; N Pos. 3,6,9,12,15
Seq#:24; Xaa Pos. 7
Seq#:31; Xaa Pos. 7
Seq#:32; Xaa Pos. 7
Seq#:33; Xaa Pos. 12
Seq#:34; Xaa Pos. 7
Seq#:36; N Pos. 18
Seq#:58; Xaa Pos. 7
Seq#:59; Xaa Pos. 7

VERIFICATION SUMMARY

DATE: 03/21/2005 PATENT APPLICATION: US/09/476,485B TIME: 14:12:05

Input Set : A:\10823619.app

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L:506 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:588 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
L:892 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
L:911 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:930 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0
L:949 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:982 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:1520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0
L:1541 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59 after pos.:0
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